

## SEQUENCE LISTING

<110> Nakamura, Toshikazu

<120> NEOVASCULARIZATION INHIBITORS

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<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 447

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> pyroglutamate

<220>

<221> CHAIN

<222> (1)..(447)

<223> N-terminal region of alpha-chain in HGF (PyrGlu32-Val478/HGF)

<400> 1

Glu Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys  
1 5 10 15

Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys  
20 25 30

Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly  
35 40 45

Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln  
50 55 60

Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu  
65 70 75 80

Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn  
85 90 95

Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr  
100 105 110

Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu  
115 120 125

His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn  
130 135 140

Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Pro Trp Cys Phe Thr  
145 150 155 160

Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser  
165 170 175

Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met  
180 185 190

Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr  
195 200 205

Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe  
210 215 220

Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys  
225 230 235 240

Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr  
245 250 255

Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr  
260 265 270

Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr  
275 280 285

Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His  
290 295 300

Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu  
305 310 315 320

Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr  
325 330 335

Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys  
340 345 350

Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr  
355 360 365

Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp  
370 375 380

Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp  
385 390 395 400

Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Ala  
405 410 415

His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr  
420 425 430

Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val  
435 440 445

<210> 2  
<211> 442  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARSPPLIC  
<222> (130)..(131)  
<223> deletion of five amino acids

<220>  
<221> CHAIN

<222> (1)..(442)

<223> N-terminal region of alpha-chain in HGF (PyrGlu32-Val478/HGF)

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> pyroglutamate

<400> 2

Glu Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys  
1 5 10 15

Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys  
20 25 30

Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly  
35 40 45

Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln  
50 55 60

Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu  
65 70 75 80

Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn  
85 90 95

Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr  
100 105 110

Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu  
115 120 125

His Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro  
130 135 140

Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val  
145 150 155 160

Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met  
165 170 175

Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser  
180 185 190

Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys  
195 200 205

Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys  
210 215 220

Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro  
225 230 235 240

His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr  
245 250 255

Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly  
260 265 270

Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile  
275 280 285

Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr  
290 295 300

Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn  
305 310 315 320

Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile  
325 330 335

Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly  
340 345 350

Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser  
355 360 365

Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu  
370 375 380

Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn  
385 390 395 400

Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His Gly Pro Trp Cys  
405 410 415

Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg  
420 425 430

Cys Glu Gly Asp Thr Thr Pro Thr Ile Val  
435 440